

SEQUENCE LISTING

<110> Von Schaewen, Antje

<120> Plant GntI Sequences and the Use Thereof for the Production
of Plants Having Reduced or Lacking N-acetyl Glucosaminyl
Transferase I(GnTI) Activity

<130> 032266-003

<140> US 09/591,466

<141> 2000-06-09

<150> EP 98/08001

<151> 1998-09-12

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1669

<212> DNA

<213> Solanum tuberosum

<220>

<221> misc_feature

<222> (659)...(667)

<223> function: Asn codon in this context is a potential
glycosylation site;

product: N-glycosylation consensus sequence;

phenotype: N-glycans modulate protein properties;

<220>

<221> misc_feature

<222> (659)...(667)

<223> standard_name: N-glycosylation site;

label: pot-CHO;

note: GnTI-coding sequences from animals do not
contain this feature.

<220>

<221> CDS

<222> (53)...(1393)

<223> codon_start: 53;

function: initiates complex N-glycans on secretory
glycoproteins;

EC_number: 2.4.1.101;

<220>

<221> CDS

<222> (53)...(1393)

<223> product: beta-1,2-N-acetylglucosaminyltransferase I;

evidence: EXPERIMENTAL;

<220>
<221> CDS
<222> (53) ... (1393)
<223> gene: cgl;
standard_name: gntI;
label: ORF;
note: first gntI sequence from potato (unpublished).

<220>
<221> 5'UTR
<222> (15) ... (52)

<220>
<221> 3'UTR
<222> (1394) ... (1655)

<220>
<221> CDS
<222> (80) ... (139)
<223> function: membrane anchor (amino acids 10-29);
product: hydrophobic amino acid stretch in GntI;
standard_name: membrane anchor of a type II Golgi
protein;

<220>
<221> CDS
<222> (80) ... (139)
<223> note: identified by comparison with GntI sequences
from animals.

<220>
<221> misc_feature
<222> (1) ... (14)
<223> function: used for cloning the cDNA library in
Lambda ZAPII;
product: EcoRI/NotI-cDNA adapter;
number: 1.

<220>
<221> misc_feature
<222> (1656) ... (1669)
<223> product: EcoRI/NotI-cDNA adapter;
number: 2.

<400> 1
gaattcgcgg ccgcctgaga aaccctcgaa ttcaatttcg catttggcag ag atg aga 58
Met Arg
1

ggg aac aag ttt tgc ttt gat tta cgg tac ctt ctc gtc gtg gct gct 106
Gly Asn Lys Phe Cys Phe Asp Leu Arg Tyr Leu Leu Val Val Ala Ala

5	10	15	
ctc gcc ttc atc tac ata cag atg cg ^g ctt ttc gc ^g aca cag tc ^a gaa Leu Ala Phe Ile Tyr Ile Gln Met Arg Leu Phe Ala Thr Gln Ser Glu	20	25	154
		30	
tat gta gac cgc ctt gct gca att gaa gca gaa aat cat tgt aca Tyr Val Asp Arg Leu Ala Ala Ile Glu Ala Glu Asn His Cys Thr	35	40	202
		45	50
agt cag acc aga ttg ctt att gac aag att agc cag cag caa gga aga Ser Gln Thr Arg Leu Leu Ile Asp Lys Ile Ser Gln Gln Gln Gly Arg	55	60	250
		65	
gta gta gct ctt gaa gaa caa atg aag cat cag gag tgc cg ^g Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu Cys Arg	70	75	298
		80	
caa tta agg gct ctt gtt cag gat ctt gaa agt aag ggc ata aaa aag Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile Lys Lys	85	90	346
		95	
tta atc gga gat gtg cag atg cca gtg gca gct gta gtt gtt atg gct Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val Val Met Ala	100	105	394
		110	
tgc agt cgt act gac tac ctg gag agg act att aaa tcc atc tta aaa Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile Leu Lys	115	120	442
		125	130
tac caa aca tct gtt gca tca aaa tat cct ctt ttc ata tcc cag gat Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln Asp	135	140	490
		145	
gga tca aat cct gat gta aga aag ctt gct ttg agc tat ggt cag ctg Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly Gln Leu	150	155	538
		160	
acg tat atg cag cac ttg gat tat gaa cct gtg cat act gaa aga cca Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu Arg Pro	165	170	586
		175	
ggg gaa ctg gtt gca tac tac aag att gca cgt cat tac aag tgg gca Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp Ala	180	185	634
		190	
ttg gat cag ctg ttt cac aag cat aat ttt agc cgt gtt atc ata cta Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile Ile Leu	195	200	682
		205	210
gaa gat gat atg gaa att gct gct gat ttt ttt gac tat ttt gag gct Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe Glu Ala	215	220	730
		225	

ggg gct act ctt ctt gac aga gac aag tcg att atg gct att tct tct Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile Ser Ser	230	235	240	778
tgg aat gac aat gga caa agg cag ttc gtc caa gat cct gat gct ctt Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp Ala Leu	245	250	255	826
tac cgc tca gac ttt ttt cct ggt ctt gga tgg atg ctt tca aaa tca Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser Lys Ser	260	265	270	874
act tgg tcc gaa cta tct cca aag tgg cca aag gct tac tgg gat gac Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp Asp	275	280	285	922
tgg cta agg ctg aaa gaa aat cac aga ggt cga caa ttt att cgc cca Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile Arg Pro	295	300	305	970
gaa gtt tgc aga acg tac aat ttt ggt gag cat ggt tct agt ttg ggg Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Ser Ser Leu Gly	310	315	320	1018
cag ttt ttt aag cag tat ctt gag cca att aag cta aat gat gtc cag Gln Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val Gln	325	330	335	1066
gtt gat tgg aag tca atg gac cta agt tac ctt ttg gag gac aac tat Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp Asn Tyr	340	345	350	1114
gtg aaa cac ttt ggc gac ttg gtt aaa aag gct aag ccc atc cac gga Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile His Gly	355	360	365	1162
gct gat gct gtt ttg aaa gca ttt aac ata gat ggt gat gtg cgt att Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val Arg Ile	375	380	385	1210
cag tac aga gac caa cta gac ttt gaa gat atc gct cga cag ttt ggc Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln Phe Gly	390	395	400	1258
att ttt gaa gaa tgg aag gat ggt gta cca cg gca gca tat aaa ggg Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr Lys Gly	405	410	415	1306
ata gta gtt ttc cg gtt ttt caa aca tct aga cgt gtg ttc ctt gtt tcc Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu Val Ser	420	425	430	1354

cct gat tct ctt cga caa ctt gga gtt gaa gat act tag cgaagatatg 1403
 Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr *
 435 440 445

attggagcct gagcaacaat ttagacttat ttggtaggat acatttgaaa gagctgacac 1463
 gaaaagtatg actaccagta gctacatgca acattttaat gttaatggaa ggaacccact 1523
 gcttattgtt ggaatggatg aatcatcacc acatcctatt attcaagttt acaaacataa 1583
 agagggaaatg ttgcctata aaaacaaatt ttttgttct aagaaggAAC gttacgatta 1643
 ttagcaactt tggcgccgc gaattc 1669

<210> 2
 <211> 446
 <212> PRT
 <213> Solanum tuberosum

<400> 2
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 1 5 10 15
 Ala Ala Leu Ala Phe Ile Tyr Ile Gln Met Arg Leu Phe Ala Thr Gln
 20 25 30
 Ser Glu Tyr Val Asp Arg Leu Ala Ala Ile Glu Ala Glu Asn His
 35 40 45
 Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Lys Ile Ser Gln Gln Gln
 50 55 60
 Gly Arg Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu
 65 70 75 80
 Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile
 85 90 95
 Lys Lys Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val Val
 100 105 110
 Met Ala Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile
 115 120 125
 Leu Lys Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser
 130 135 140
 Gln Asp Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly
 145 150 155 160
 Gln Leu Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu
 165 170 175
 Arg Pro Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys
 180 185 190
 Trp Ala Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile
 195 200 205
 Ile Leu Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe
 210 215 220
 Glu Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile
 225 230 235 240
 Ser Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp
 245 250 255
 Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser
 260 265 270
 Lys Ser Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp
 275 280 285
 Asp Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile

290	295	300
Arg Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser		
305	310	315
Leu Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp		
325	330	335
Val Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp		
340	345	350
Asn Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile		
355	360	365
His Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val		
370	375	380
Arg Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln		
385	390	395
Phe Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr		
405	410	415
Lys Gly Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu		
420	425	430
Val Ser Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr		
435	440	445

<210> 3

<211> 1737

<212> DNA

<213> Nicotiana tabacum

<220>

<221> misc_feature

<222> (733)...(741)

<223> function: Asn codon in this context is a potential glycosylation site;
 product: N-glycosylation consensus sequence;
 phenotype: N-glycans modulate protein properties;

<220>

<221> misc_feature

<222> (733)...(741)

<223> standard_name: N-glycosylation site;
 label: pot-CHO;
 note: GnTI sequences from animals do not contain
 this feature.

<220>

<221> CDS

<222> (127)...(1467)

<223> codon_start: 127;
 function: initiates complex N-glycans on secretory
 glycoproteins;
 EC_number: 2.4.1.101;

<220>

<221> CDS

<222> (127) ... (1467)
 <223> product: beta-1,2-N-acetylglucosaminlytransferase I;
 evidence: EXPERIMENTAL;
 gene: cgl;
 standard_name: gntI;

<220>
 <221> CDS
 <222> (127) ... (1467)
 <223> label: ORF;
 note: first gntI sequence from tobacco (unpublished).

<220>
 <221> 5'UTR
 <222> (15) ... (126)

<220>
 <221> 3'UTR
 <222> (1468) ... (1723)

<220>
 <221> CDS
 <222> (154) ... (213)
 <223> function: membrane anchor (amino acids 10-29);
 product: hydrophobic amino acid stretch in GntI;
 standard_name: membrane anchor of a type II golgi
 protein.

<220>
 <221> misc_feature
 <222> (1) ... (14)
 <223> function: use for cloning the cDNA library in
 Lambda ZAPII;
 product: EcoRI/NotI-cDNA adapter;
 number: 1.

<220>
 <221> misc_feature
 <222> (1724) ... (1737)
 <223> product: EcoRI/NotI-cDNA adapter;
 number: 2.

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 aacactcata actgaacact gagagactat tcgccttctc ctaaagcctt caatcgaaatt 120
 cgcacg atg aga ggg aac aag ttt tgc tgt gat ttc cgg tac ctc ctc 168
 Met Arg Gly Asn Lys Phe Cys Cys Asp Phe Arg Tyr Leu Leu
 1 5 10

atc ttg gct gtc gcc ttc atc tac aca cag atg cgg ctt ttt gcg 216
 Ile Leu Ala Ala Val Ala Phe Ile Tyr Thr Gln Met Arg Leu Phe Ala
 15 20 25 30

aca cag tca gaa tat gca gat cgc ctt gct gca att gaa gca gaa		264	
Thr Gln Ser Glu Tyr Ala Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu			
35	40	45	
aat cat tgt aca agc cag acc aga ttg ctt att gac cag att agc ctg		312	
Asn His Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Gln Ile Ser Leu			
50	55	60	
cag caa gga aga ata gtt gct ctt gaa gaa caa atg aag cgt cag gac		360	
Gln Gln Gly Arg Ile Val Ala Leu Glu Gln Met Lys Arg Gln Asp			
65	70	75	
cag gag tgc cga caa tta agg gct ctt gtt cag gat ctt gaa agt aag		408	
Gln Glu Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys			
80	85	90	
ggc ata aaa aag ttg atc gga aat gta cag atg cca gtg gct gct gta		456	
Gly Ile Lys Lys Leu Ile Gly Asn Val Gln Met Pro Val Ala Ala Val			
95	100	105	110
gtt gtt atg gct tgc aat cgg gct gat tac ctg gaa aag act att aaa		504	
Val Val Met Ala Cys Asn Arg Ala Asp Tyr Leu Glu Lys Thr Ile Lys			
115	120	125	
tcc atc tta aaa tac caa ata tct gtt gcg tca aaa tat cct ctt ttc		552	
Ser Ile Leu Lys Tyr Gln Ile Ser Val Ala Ser Lys Tyr Pro Leu Phe			
130	135	140	
ata tcc cag gat gga tca cat cct gat gtc agg aag ctt gct ttg agc		600	
Ile Ser Gln Asp Gly Ser His Pro Asp Val Arg Lys Leu Ala Leu Ser			
145	150	155	
tat gat cag ctg acg tat atg cag cac ttg gat ttt gaa cct gtg cat		648	
Tyr Asp Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val His			
160	165	170	
act gaa aga cca ggg gag ctg att gca tac tac aaa att gca cgt cat		696	
Thr Glu Arg Pro Gly Glu Leu Ile Ala Tyr Tyr Lys Ile Ala Arg His			
175	180	185	190
tac aag tgg gca ttg gat cag ctg ttt tac aag cat aat ttt agc cgt		744	
Tyr Lys Trp Ala Leu Asp Gln Leu Phe Tyr Lys His Asn Phe Ser Arg			
195	200	205	
gtt atc ata cta gaa gat gat atg gaa att gcc cct gat ttt ttt gac		792	
Val Ile Ile Leu Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp			
210	215	220	
ttt ttt gag gct gga gct act ctt gac aga gac aag tcg att atg		840	
Phe Phe Glu Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met			
225	230	235	
gct att tct tct tgg aat gac aat gga caa atg cag ttt gtc caa gat		888	

Ala Ile Ser Ser Trp Asn Asp Asn Gly Gln Met Gln Phe Val Gln Asp			
240	245	250	
cct tat gct ctt tac cgc tca gat ttt ttt ccc ggt ctt gga tgg atg			936
Pro Tyr Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met			
255	260	265	270
ctt tca aaa tct act tgg gac gaa tta tct cca aag tgg cca aag gct			984
Leu Ser Lys Ser Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala			
275	280	285	
tac tgg gac gac tgg cta aga ctc aaa gag aat cac aga ggt cga caa			1032
Tyr Trp Asp Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln			
290	295	300	
ttt att cgc cca gaa gtt tgc aga aca tat aat ttt ggt gag cat ggt			1080
Phe Ile Arg Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly			
305	310	315	
tct agt ttg ggg cag ttt ttc aag cag tat ctt gag cca att aaa cta			1128
Ser Ser Leu Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu			
320	325	330	
aat gat gtc cag gtt gat tgg aag tca atg gac ctt agt tac ctt ttg			1176
Asn Asp Val Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu			
335	340	345	350
gag gac aat tac gtg aaa cac ttt ggt gac ttg gtt aaa aag gct aag			1224
Glu Asp Asn Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys			
355	360	365	
ccc atc cat gga gct gat gct gtc ttg aaa gca ttt aac ata gat ggt			1272
Pro Ile His Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly			
370	375	380	
gat gtg cgt att cag tac aga gatcaa cta gac ttt gaa aat atc gca			1320
Asp Val Arg Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asn Ile Ala			
385	390	395	
cgg caa ttt ggc att ttt gaa gaa tgg aag gat ggt gta cca cgt gca			1368
Arg Gln Phe Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala			
400	405	410	
gca tat aaa gga ata gta gtt ttc cgg tac caa acg tcc aga cgt gta			1416
Ala Tyr Lys Gly Ile Val Val Phe Arg Tyr Gln Thr Ser Arg Arg Val			
415	420	425	430
ttc ctt gtt ggc cat gat tcg ctt caa caa ctc gga att gaa gat act			1464
Phe Leu Val Gly His Asp Ser Leu Gln Gln Leu Gly Ile Glu Asp Thr			
435	440	445	
taa caaagatatg attgcaggag cccgggcaaa atttttgact tattggtag			1517
*			

gatgcacatcgaa gctgacacta aaccatgatt ttaccaggta catacaacgt tttaatgtta 1577
 tacggaggag ctcactgttc tagtgttcaa gggatatcgg cttcttagta ttggatgaat 1637
 catcaacaca acctattatt ttaagtgttc agaacataaa gaggaaatgt agccctgtaa 1697
 agactataca tgggaccatc ataatcgccg cccgcaattc 1737

<210> 4
<211> 446
<212> PRT
<213> Nicotiana tabacum

<400> 4
 Met Arg Gly Asn Lys Phe Cys Cys Asp Phe Arg Tyr Leu Leu Ile Leu
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 20 25 30
 Ser Glu Tyr Ala Asp Arg Leu Ala Ala Ile Glu Ala Glu Asn His
 35 40 45
 Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Gln Ile Ser Leu Gln Gln
 50 55 60
 Gly Arg Ile Val Ala Leu Glu Glu Gln Met Lys Arg Gln Asp Gln Glu
 65 70 75 80
 Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile
 85 90 95
 Lys Lys Leu Ile Gly Asn Val Gln Met Pro Val Ala Ala Val Val Val
 100 105 110
 Met Ala Cys Asn Arg Ala Asp Tyr Leu Glu Lys Thr Ile Lys Ser Ile
 115 120 125
 Leu Lys Tyr Gln Ile Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser
 130 135 140
 Gln Asp Gly Ser His Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Asp
 145 150 155 160
 Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val His Thr Glu
 165 170 175
 Arg Pro Gly Glu Leu Ile Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys
 180 185 190
 Trp Ala Leu Asp Gln Leu Phe Tyr Lys His Asn Phe Ser Arg Val Ile
 195 200 205
 Ile Leu Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp Phe Phe
 210 215 220
 Glu Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile
 225 230 235 240
 Ser Ser Trp Asn Asp Asn Gly Gln Met Gln Phe Val Gln Asp Pro Tyr
 245 250 255
 Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser
 260 265 270
 Lys Ser Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp
 275 280 285
 Asp Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile
 290 295 300
 Arg Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser
 305 310 315 320
 Leu Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp

	325	330	335
Val Gln Val Asp Trp Lys Ser Met	Asp Leu Ser Tyr Leu Leu	Glu Asp	
340	345	350	
Asn Tyr Val Lys His Phe Gly Asp	Leu Val Lys Lys Ala Lys Pro Ile		
355	360	365	
His Gly Ala Asp Ala Val Leu Lys	Ala Phe Asn Ile Asp Gly Asp Val		
370	375	380	
Arg Ile Gln Tyr Arg Asp Gln Leu Asp	Phe Glu Asn Ile Ala Arg Gln		
385	390	395	400
Phe Gly Ile Phe Glu Glu Trp Lys Asp	Gly Val Pro Arg Ala Ala Tyr		
405	410	415	
Lys Gly Ile Val Val Phe Arg Tyr Gln	Thr Ser Arg Arg Val Phe Leu		
420	425	430	
Val Gly His Asp Ser Leu Gln Gln	Leu Gly Ile Glu Asp Thr		
435	440	445	

<210> 5
<211> 1854
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1185) ... (1193)
<223> function: Asn Codon is a potential glycosylation site;
product: Consensus sequence for N-glycosylation;
phenotype: N glycans modulate protein characteristics;
standard name: N glycosylation site;

<220>
<221> misc_feature
<222> (1185) ... (1193)
<223> label: pot-CHO;
note: absent in animal GnTI sequences.

<220>
<221> CDS
<222> (135) ... (1469)
<223> codon_start: 135;
function: initiates complex N glycans on secretory glycoproteins;
EC_number: 2.4.1.101;
<220>
<221> CDS
<222> (135) ... (1469)
<223> product: beta-1,2-N-acetyl glucosaminyl transferase I;
evidence: EXPERIMENTAL;
gene: cgl;
standard_name: gntI;

<220>
<221> CDS
<222> (135) ... (1469)
<223> label: ORF;

note: first gntI sequence from Arabidopsis
(unpublished).

<220>
<221> 5'UTR
<222> (19) ... (134)

<220>
<221> 3'UTR
<222> (1470) ... (1848)

<220>
<221> CDS
<222> (157) ... (215)
<223> function: membrane anchor (amino acids 8-27);
product: hydrophobic amino-acid region in GnTI;
standard_name: membrane anchor of a Type II Golgi protein;
note: identified by comparison with animal GnTI sequences.

<220>
<221> misc_feature
<222> (1) ... (18)
<223> function: for preparation of a cDNA library in
Lambda ACT;
product: XhoI-cDNA-Adaptor;
number: 1.

<220>
<221> misc_feature
<222> (1849) ... (1854)
<223> product: XhoI-cDNA-Adaptor;
number: 2.

<400> 5
ctcgaggcca cgaaggccac cgaaaaatataacgaacg acaccgttcc aaacaacttc 60
cttattagct agctccctcc cggcggcaaa caccagaaga tccaccgctt ttgatctgg 120
tgtttgcgtt ccat atg gcg agg atc tcg tgt gac ttg aga tt ctt ctc 170
Met Ala Arg Ile Ser Cys Asp Leu Arg Phe Leu Leu
1 5 10

atc ccg gca gct ttc atg ttc atc tac atc cag atg agg ctt ttc cag	218
Ile Pro Ala Ala Phe Met Phe Ile Tyr Ile Gln Met Arg Leu Phe Gln	
15 20 25	

acg caa tca cag tat gca gat cgc ctc agt tcc gct atc gaa tct gag	266
Thr Gln Ser Gln Tyr Ala Asp Arg Leu Ser Ser Ala Ile Glu Ser Glu	
30 35 40	

aac cat tgc act agt caa atg cga ggc ctc ata gat gaa gtt agc atc	314
Asn His Cys Thr Ser Gln Met Arg Gly Leu Ile Asp Glu Val Ser Ile	
45 50 55 60	

aaa cag tcg cgg att gtt gcc ctc gaa gat atg aag aac cgc cag gac	362
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Lys Gln Ser Arg Ile Val Ala Leu Glu Asp Met Lys Asn Arg Gln Asp			
65	70	75	
gaa gaa ctt gtg cag ctt aag gat cta atc cag acg ttt gaa aaa aaa			
Glu Glu Leu Val Gln Leu Lys Asp Leu Ile Gln Thr Phe Glu Lys Lys			410
80	85	90	
gga ata gca aaa ctc act caa ggt gga cag atg cct gtg gct gct gta			
Gly Ile Ala Lys Leu Thr Gln Gly Gln Met Pro Val Ala Ala Val			458
95	100	105	
gtg gtt atg gcc tgc agt cgt gca gac tat ctt gaa agg act gtt aaa			
Val Val Met Ala Cys Ser Arg Ala Asp Tyr Leu Glu Arg Thr Val Lys			506
110	115	120	
tca gtt tta aca tat caa act ccc gtt gct tca aaa tat cct cta ttt			
Ser Val Leu Thr Tyr Gln Thr Pro Val Ala Ser Lys Tyr Pro Leu Phe			554
125	130	135	140
ata tct cag gat gga tct gat caa gct gtc aag agc aag tca ttg agc			
Ile Ser Gln Asp Gly Ser Asp Gln Ala Val Lys Ser Lys Ser Leu Ser			602
145	150	155	
tat aat caa tta aca tat atg cag cac ttg gat ttt gaa cca gtg gtc			
Tyr Asn Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val Val			650
160	165	170	
act gaa agg cct ggt gaa ctg act gcg tac tac aag att gca cgt cac			
Thr Glu Arg Pro Gly Glu Leu Thr Ala Tyr Tyr Lys Ile Ala Arg His			698
175	180	185	
tac aag tgg gca ctg gac cag ttg ttt tac aaa cac aaa ttt agt cga			
Tyr Lys Trp Ala Leu Asp Gln Leu Phe Tyr Lys His Lys Phe Ser Arg			746
190	195	200	
gtg att ata cta gaa gac gat atg gaa att gct cca gac ttc ttt gat			
Val Ile Ile Leu Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp			794
205	210	215	220
tac ttt gag gct gca gct agt ctc atg gat agg gat aaa acc att atg			
Tyr Phe Glu Ala Ala Ala Ser Leu Met Asp Arg Asp Lys Thr Ile Met			842
225	230	235	
gct gct tca tca tgg aat gat aat gga cag aag cag ttt gtg cat gat			
Ala Ala Ser Ser Trp Asn Asp Asn Gly Gln Lys Gln Phe Val His Asp			890
240	245	250	
ccc tat gcg cta tac cga tca gat ttt ttt cct ggc ctt ggg tgg atg			
Pro Tyr Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met			938
255	260	265	
ctc aag aga tcg act tgg gat gag tta tca cca aag tgg cca aag gct			
Leu Lys Arg Ser Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala			986

270	275	280	
tac tgg gat gat tgg ctg aga cta aag gaa aac cat aaa ggc cgc caa Tyr Trp Asp Asp Trp Leu Arg Leu Lys Glu Asn His Lys Gly Arg Gln 285 290 295 300			1034
ttc att gca ccg gaa gtc tgt aga aca tac aat ttt ggt gaa cat ggg Phe Ile Ala Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly 305 310 315			1082
tct agt ttg gga cag ttt ttc agt cag tat ctg gaa cct ata aag cta Ser Ser Leu Gly Gln Phe Phe Ser Gln Tyr Leu Glu Pro Ile Lys Leu 320 325 330			1130
aac gat gtg acg gtt gac tgg aaa gca aag gac ctg gga tac ctg aca Asn Asp Val Thr Val Asp Trp Lys Ala Lys Asp Leu Gly Tyr Leu Thr 335 340 345			1178
gag gga aac tat acc aag tac ttt tct ggc tta gtg aga caa gca cga Glu Gly Asn Tyr Thr Lys Tyr Phe Ser Gly Leu Val Arg Gln Ala Arg 350 355 360			1226
cca att .caa ggt tct gac ctt gtc tta aag gct caa aac ata aag gat Pro Ile Gln Gly Ser Asp Leu Val Leu Lys Ala Gln Asn Ile Lys Asp 365 370 375 380			1274
gat gat cgt atc cgg tat aaa gac caa gta gag ttt gaa cgc att gca Asp Asp Arg Ile Arg Tyr Lys Asp Gln Val Glu Phe Glu Arg Ile Ala 385 390 395			1322
ggg gaa ttt ggt ata ttt gaa gaa tgg aag gat ggt gtg cca cga aca Gly Glu Phe Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Thr 400 405 410			1370
gca tat aaa gga gta gtg gtg ttt cga atc cag aca aca aga cgt gta Ala Tyr Lys Gly Val Val Phe Arg Ile Gln Thr Thr Arg Arg Val 415 420 425			1418
ttc ctg gtt ggg cca gat tct gta atg cag ctt gga att cga aat tcc Phe Leu Val Gly Pro Asp Ser Val Met Gln Leu Gly Ile Arg Asn Ser 430 435 440			1466
tga tgcaaaacat atgaaaaggaa aagaagattt tggaccgcat gcagcctcct			1519
*			
tcttagcagct gtttagtttgt attgttattt atggatgagt ttgttagagcg gtggggtaa ctttaacagc aaggaagctc tggtgaccag gctgattggc tttagaagttt tggaaacccc ttgaaaagggt cagggttaaa tatatttcag ttgtttattt agtgattatc ttgtggtaa cttatacgaa tgcaaatcat tctatgcagt ttttcttcgt cccacttgtt ttggcttc tattgctagt gtacatatct cttcaaaacat gtactaaata atgcgttttgc tttcaaaagaa gtaactttta ttaaaaaaaaaaaaaaac tcgag			1579 1639 1699 1759 1819 1854

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<212> PRT
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Phe Met Phe Ile Tyr Ile Gln Met Arg Leu Phe Gln Thr Gln Ser Gln
20 25 30
Tyr Ala Asp Arg Leu Ser Ser Ala Ile Glu Ser Glu Asn His Cys Thr
35 40 45
Ser Gln Met Arg Gly Leu Ile Asp Glu Val Ser Ile Lys Gln Ser Arg
50 55 60
Ile Val Ala Leu Glu Asp Met Lys Asn Arg Gln Asp Glu Glu Leu Val
65 70 75 80
Gln Leu Lys Asp Leu Ile Gln Thr Phe Glu Lys Lys Gly Ile Ala Lys
85 90 95
Leu Thr Gln Gly Gly Gln Met Pro Val Ala Ala Val Val Val Met Ala
100 105 110
Cys Ser Arg Ala Asp Tyr Leu Glu Arg Thr Val Lys Ser Val Leu Thr
115 120 125
Tyr Gln Thr Pro Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln Asp
130 135 140
Gly Ser Asp Gln Ala Val Lys Ser Lys Ser Leu Ser Tyr Asn Gln Leu
145 150 155 160
Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val Val Thr Glu Arg Pro
165 170 175
Gly Glu Leu Thr Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp Ala
180 185 190
Leu Asp Gln Leu Phe Tyr Lys His Lys Phe Ser Arg Val Ile Ile Leu
195 200 205
Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp Tyr Phe Glu Ala
210 215 220
Ala Ala Ser Leu Met Asp Arg Asp Lys Thr Ile Met Ala Ala Ser Ser
225 230 235 240
Trp Asn Asp Asn Gly Gln Lys Gln Phe Val His Asp Pro Tyr Ala Leu
245 250 255
Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Lys Arg Ser
260 265 270
Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp Asp
275 280 285
Trp Leu Arg Leu Lys Glu Asn His Lys Gly Arg Gln Phe Ile Ala Pro
290 295 300
Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu Gly
305 310 315 320
Gln Phe Phe Ser Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val Thr
325 330 335
Val Asp Trp Lys Ala Lys Asp Leu Gly Tyr Leu Thr Glu Gly Asn Tyr
340 345 350
Thr Lys Tyr Phe Ser Gly Leu Val Arg Gln Ala Arg Pro Ile Gln Gly
355 360 365
Ser Asp Leu Val Leu Lys Ala Gln Asn Ile Lys Asp Asp Asp Arg Ile

370	375	380
Arg Tyr Lys Asp Gln Val Glu Phe Glu Arg Ile Ala Gly Glu Phe Gly		
385	390	395
Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Thr Ala Tyr Lys Gly		
	405	410
Val Val Val Phe Arg Ile Gln Thr Thr Arg Arg Val Phe Leu Val Gly		
	420	425
Pro Asp Ser Val Met Gln Leu Gly Ile Arg Asn Ser		
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<220>
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<223> n at positions 6, 9 & 12 = inosine.

<400> 7
tgygynwsng cntggmayga yaay

24

<210> 8
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<223> n at positions 4, 7, & 10 = inosine.

<220>
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<222> 13
<223> n = a, c, g, or t.

<400> 8
ccanccntrn ccngsraara artc

24

<210> 9
<211> 14
<212> PRT
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<220>

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<222> 2

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<220>
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Gln Xaa Gln Phe Val Gln Asp Pro Xaa Ala Leu Tyr Arg Ser
1 5 10

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51

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<223> Primer for cloning plant genes

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40

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<400> 14

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37